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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/081,775

DATE: 03/20/2002

TIME: 11:25:58

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\03202002\J081775.raw

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3 <110> APPLICANT: Bristol-Myers Squibb Company
5 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED
6 RECEPTOR, HGPRBMY25, EXPRESSED HIGHLY IN IMMUNE-RELATED TISSUES
8 <130> FILE REFERENCE: D0126 NP
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/081,775
C--> 10 <141> CURRENT FILING DATE: 2002-02-21
10 <150> PRIOR APPLICATION NUMBER: US 60/270,134
11 <151> PRIOR FILING DATE: 2001-02-21
13 <150> PRIOR APPLICATION NUMBER: US 60/278,952
14 <151> PRIOR FILING DATE: 2001-03-27
16 <160> NUMBER OF SEQ ID NOS: 69
18 <170> SOFTWARE: PatentIn version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1567
22 <212> TYPE: DNA
23 <213> ORGANISM: homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (537)..(1523)
29 <400> SEQUENCE: 1
30 ccacgcgtcc gataattact aagtacaggg tcccaaatta gaatctattc caacttaaag      60
32 gacaagaaaa aaaaagtcca agattaccca gtgaactatg tttgtagttt gtgtcaccaa      120
34 actgatagtc acgcctaatt tcttcttata ctccataaaa gacagtgtgt atgtatgtgt      180
36 gtgtgtttct ttgtgtgtat gtatgtattc aggtatatgt gtatagcctt agctaggaga      240
38 caattctagt ttattctaaag gcttatttga gccctttctc acgttcattt attttattta      300
40 ataagcatta tatatcaggt attattcaaa gctctttaga aatctttaga catattaacc      360
42 catataattc tcttctctat agggaaataga tatgattatt attgctattt tatggatgat      420
44 gaagctttct aaacatgta tagccagtaa gtgttactat tctctcattc ctatctctgt      480
46 tctatcttgt tctccagat aatgtgatac tatgtggagg tttctgacca cagaga atg      539
47 Met
48 1
50 tcc agc act ctt ggc cac aac atg gaa tct cct cat cac act gat gtt      587
51 Ser Ser Thr Leu Gly His Asn Met Glu Ser Pro His His Thr Asp Val
52 5 10 15
54 gac cct tct gtc ttc ttc ctc ctg ggc atc cca ggt ctg gaa caa ttt      635
55 Asp Pro Ser Val Phe Phe Leu Leu Gly Ile Pro Gly Leu Glu Gln Phe
56 20 25 30
58 cat ttg tgg ctc tca ctc cct gtg tgt ggc tta ggc aca gcc aca att      683
59 His Leu Trp Leu Ser Leu Pro Val Cys Gly Leu Gly Thr Ala Thr Ile
60 35 40 45
62 gtg ggc aat ata act att ctg gtt gtt gtt gcc act gaa cca gtc ttg      731
63 Val Gly Asn Ile Thr Ile Leu Val Val Val Ala Thr Glu Pro Val Leu
64 50 55 60 65

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66 cac aag cct gtg tac ctt ttt ctg tgc atg ctc tca acc atc gac ttg      779
67 His Lys Pro Val Tyr Leu Phe Leu Cys Met Leu Ser Thr Ile Asp Leu
68      70      75      80
70 gct gcc tct gtc tcc aca gtt ccc aag cta ctg gct atc ttc tgg tgt      827
71 Ala Ala Ser Val Ser Thr Val Pro Lys Leu Leu Ala Ile Phe Trp Cys
72      85      90      95
74 gga gcc gga cat ata tct gcc tct gcc tgc ctg gca cat atg ttc ttc      875
75 Gly Ala Gly His Ile Ser Ala Ser Ala Cys Leu Ala His Met Phe Phe
76      100      105      110
78 att cat gcc ttc tgc atg atg gag tcc act gtg cta ctg gcc atg gcc      923
79 Ile His Ala Phe Cys Met Met Glu Ser Thr Val Leu Leu Ala Met Ala
80      115      120      125
82 ttt gat cgc tac gtg gcc atc tgc cac cca ctc cgc tat gcc aca atc      971
83 Phe Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Ala Thr Ile
84 130      135      140      145
86 ctc act gac acc atc att gcc cac ata ggg gtg gca gct gta gtg cga      1019
87 Leu Thr Asp Thr Ile Ile Ala His Ile Gly Val Ala Ala Val Val Arg
88      150      155      160
90 ggc tcc ctg ctc atg ctc cca tgt ccc ttc ttt att ggg cgt ttg aac      1067
91 Gly Ser Leu Leu Met Leu Pro Cys Pro Phe Phe Ile Gly Arg Leu Asn
92      165      170      175
94 ttc tgc caa agc cat gtg atc cta cac acg tac tgt gag cac atg gct      1115
95 Phe Cys Gln Ser His Val Ile Leu His Thr Tyr Cys Glu His Met Ala
96      180      185      190
98 gtg gtg aag ctg gcc tgt gga gac acc agg cct aac cgt gtg tat ggg      1163
99 Val Val Lys Leu Ala Cys Gly Asp Thr Arg Pro Asn Arg Val Tyr Gly
100      195      200      205
102 ctg aca gct gca ctg ttg gtc att ggg gtt gac ttg ttt tgc att ggt      1211
103 Leu Thr Ala Ala Leu Leu Val Ile Gly Val Asp Leu Phe Cys Ile Gly
104 210      215      220      225
106 ctc tcc tat gcc cta att gca caa gct gtc ctt cgc ctc tca tcc cat      1259
107 Leu Ser Tyr Ala Leu Ile Ala Gln Ala Val Leu Arg Leu Ser Ser His
108      230      235      240
110 gaa gct cgg tcc aag gcc cta ggg acc tgt ggt tcc cat gtc tgt gtc      1307
111 Glu Ala Arg Ser Lys Ala Leu Gly Thr Cys Gly Ser His Val Cys Val
112      245      250      255
114 atc ctc atc tct tat aca cca gcc ctc ttc tcc ttt ttt aca cac cgc      1355
115 Ile Leu Ile Ser Tyr Thr Pro Ala Leu Phe Ser Phe Phe Thr His Arg
116      260      265      270
118 ttt ggc cat cac gtt cca gtc cat att cac att ctt ttg gcc aat gtt      1403
119 Phe Gly His His Val Pro Val His Ile His Ile Leu Leu Ala Asn Val
120      275      280      285
122 tat ctg ctt ttg cca cct gct ctt aat cct gtg gta tat gga gtt aag      1451
123 Tyr Leu Leu Leu Pro Pro Ala Leu Asn Pro Val Val Tyr Gly Val Lys
124 290      295      300      305
126 acc aaa cag atc cgt aaa aga gtt gtc agg gtg ttt caa agt ggg cag      1499
127 Thr Lys Gln Ile Arg Lys Arg Val Val Arg Val Phe Gln Ser Gly Gln
128      310      315      320
130 gga atg ggc atc aag gca tct gag tgaccctgga gtatagaggg acttaatcca      1553

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1567

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131 Gly Met Gly Ile Lys Ala Ser Glu
132          325
134 aaaaaaaaaa aaaa
137 <210> SEQ ID NO: 2
138 <211> LENGTH: 329
139 <212> TYPE: PRI
140 <213> ORGANISM: homo sapiens
142 <400> SEQUENCE: 2
144 Met Ser Ser Thr Leu Gly His Asn Met Glu Ser Pro His His Thr Asp
145 1          5          10          15
148 Val Asp Pro Ser Val Phe Phe Leu Leu Gly Ile Pro Gly Leu Glu Gln
149          20          25          30
152 Phe His Leu Trp Leu Ser Leu Pro Val Cys Gly Leu Gly Thr Ala Thr
153          35          40          45
156 Ile Val Gly Asn Ile Thr Ile Leu Val Val Val Ala Thr Glu Pro Val
157          50          55          60
160 Leu His Lys Pro Val Tyr Leu Phe Leu Cys Met Leu Ser Thr Ile Asp
161 65          70          75          80
164 Leu Ala Ala Ser Val Ser Thr Val Pro Lys Leu Leu Ala Ile Phe Trp
165          85          90          95
168 Cys Gly Ala Gly His Ile Ser Ala Ser Ala Cys Leu Ala His Met Phe
169          100         105         110
172 Phe Ile His Ala Phe Cys Met Met Glu Ser Thr Val Leu Leu Ala Met
173          115         120         125
176 Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Ala Thr
177          130         135         140
180 Ile Leu Thr Asp Thr Ile Ile Ala His Ile Gly Val Ala Ala Val Val
181 145         150         155         160
184 Arg Gly Ser Leu Leu Met Leu Pro Cys Pro Phe Phe Ile Gly Arg Leu
185         165         170         175
188 Asn Phe Cys Gln Ser His Val Ile Leu His Thr Tyr Cys Glu His Met
189         180         185         190
192 Ala Val Val Lys Leu Ala Cys Gly Asp Thr Arg Pro Asn Arg Val Tyr
193         195         200         205
196 Gly Leu Thr Ala Ala Leu Leu Val Ile Gly Val Asp Leu Phe Cys Ile
197         210         215         220
200 Gly Leu Ser Tyr Ala Leu Ile Ala Gln Ala Val Leu Arg Leu Ser Ser
201 225         230         235         240
204 His Glu Ala Arg Ser Lys Ala Leu Gly Thr Cys Gly Ser His Val Cys
205         245         250         255
208 Val Ile Leu Ile Ser Tyr Thr Pro Ala Leu Phe Ser Phe Phe Thr His
209         260         265         270
212 Arg Phe Gly His His Val Pro Val His Ile His Ile Leu Leu Ala Asn
213         275         280         285
216 Val Tyr Leu Leu Leu Pro Pro Ala Leu Asn Pro Val Val Tyr Gly Val
217         290         295         300
220 Lys Thr Lys Gln Ile Arg Lys Arg Val Val Arg Val Phe Gln Ser Gly
221 305         310         315         320
224 Gln Gly Met Gly Ile Lys Ala Ser Glu

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225                               325
228 <210> SEQ ID NO: 3
229 <211> LENGTH: 320
230 <212> TYPE: PRT
231 <213> ORGANISM: Rattus norvegicus
233 <400> SEQUENCE: 3
235 Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Met Leu Ile Gly Ile
236 1                               5                               10                               15
238 Pro Gly Leu Glu Glu Ala His Phe Trp Phe Gly Phe Pro Leu Leu Ser
239                               20                               25                               30
241 Met Tyr Ala Val Ala Leu Phe Gly Asn Cys Ile Val Val Phe Ile Val
242                               35                               40                               45
244 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
245                               50                               55                               60
247 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
248 65                               70                               75                               80
250 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Thr Phe Asp Ala Cys
251                               85                               90                               95
253 Leu Ala Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
254                               100                              105                              110
256 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
257                               115                              120                              125
259 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Val Gln Ile Gly
260                               130                              135                              140
262 Met Val Ala Leu Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
263 145                              150                              155                              160
265 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
266                               165                              170                              175
268 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Thr Asp Thr Leu
269                               180                              185                              190
271 Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
272                               195                              200                              205
274 Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Ala Val
275                               210                              215                              220
277 Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
278 225                              230                              235                              240
280 Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
281                               245                              250                              255
283 Leu Ser Val Val His Arg Phe Gly Asn Ser Leu Asp Pro Ile Val His
284                               260                              265                              270
286 Val Leu Met Gly Asp Val Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
287                               275                              280                              285
289 Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
290                               290                              295                              300
292 Met Phe Lys Ile Ser Cys Asp Lys Asp Ile Glu Ala Gly Gly Asn Thr
293 305                              310                              315                              320
295 <210> SEQ ID NO: 4
296 <211> LENGTH: 320
297 <212> TYPE: PRT

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298 <213> ORGANISM: homo sapiens
300 <400> SEQUENCE: 4
302 Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile
303 1 5 10 15
305 Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
306 20 25 30
308 Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
309 35 40 45
311 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
312 50 55 60
314 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
315 65 70 75 80
317 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys
318 85 90 95
320 Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
321 100 105 110
323 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
324 115 120 125
326 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
327 130 135 140
329 Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
330 145 150 155 160
332 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
333 165 170 175
335 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
336 180 185 190
338 Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
339 195 200 205
341 Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
342 210 215 220
344 Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
345 225 230 235 240
347 Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
348 245 250 255
350 Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg
351 260 265 270
353 Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
354 275 280 285
356 Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
357 290 295 300
359 Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln Ala Val Gly Gly Lys
360 305 310 315 320
362 <210> SEQ ID NO: 5
363 <211> LENGTH: 318
364 <212> TYPE: PRT
365 <213> ORGANISM: homo sapiens
367 <400> SEQUENCE: 5
369 Met Ser Asp Ser Asn Leu Ser Asp Asn His Leu Pro Asp Thr Phe Phe
370 1 5 10 15

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VERIFICATION SUMMARY

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TIME: 11:25:59

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\03202002\J081775.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date